



(TM)

Release 3.1A John F. Collins, Biocomputing Research Unit.
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MSrch_n n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Tue Dec 28 17:36:04 1999; MasPar time 4711.84 Seconds

1403.358 Million cell updates/sec

Tabular output not generated.

Title: >US-09-327-230-1
Description: (1-2822) from US09327230.seq
Perfect Score: 2822
N.A. Sequence: 1 gcaacgcacacacagagca.....tccacgttggtggttcgq 2822
Comp: cgttcgtgtgtgttcgtcgt.....aagtcacacacacacaccc

Scoring table: TABLE default

Gap 6

Mismatch STD: Dbase 0; Query 0

Searched: 2883791 seqs, 1171580779 bases x 2

Post-processing: Minimum Match 08

Listing first 45 summaries

Database: emb1_est18
1:em_est10 2:em_est11 3:em_est17 4:em_est18 5:em_est2

Database: genbank_est11

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Statistics: Mean 12.348; Variance 2.671; scale 4.623

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	58	2.1	252	17	AA754459	97SN1787 Rice Immature	4.07e-49
2	59	2.1	252	17	AA754459	97SN1787 Rice Immature	1.04e-50
3	53	1.9	247	17	AA754458	97SN1784 Rice Immature	2.90e-41
4	49	1.7	247	17	AA754458	97SN1784 Rice Immature	3.91e-35
5	44	1.6	247	17	AA754458	97SN1784 Rice Immature	1.06e-27
6	44	1.6	247	17	AA754458	97SN1784 Rice Immature	1.06e-27
7	39	1.4	2275	20	AF034173	Human mRNA (T	7.77e-18
8	37	1.3	2275	20	AF034173	Human mRNA (T	1.40e-20
9	27	1.0	250	16	AA633452	np62b07.s1 NCI CGAP Br	2.38e-05
10	27	1.0	301	20	AA846497	a185901.s1 Soares_Para	2.38e-05

LOCUS	1	252 bp	mRNA	20-JAN-1998
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/notes=Vector: pBluescript SK(+), Site_1: EcoRI, Site_2:
XhoI; Directional cDNA library inserted into lambda ZAPII
vector at 5' end with EcoRI and 3' end with Xho I site."
/db_xref="taxon:4530"
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/clone_lib="Rice Immature Seed Lambda ZAPII cDNA library"
/tissue_type="Immature Seed"
/dev_stage="5 days after pollination"
/lab_host="E. coli SOLR"

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	Query Match	2.1%	Score 58;	DB 17;	Length 252;
	Best Local Similarity	10.8%	Pred. No.	4, 07e-49;	
	Matches	23;	Conservative	110;	Mismatches 78; Indels 2; Gaps 2;
Dd	20	TTSYBCHGNBYWVCVASHGNTMSVHNCBTBRGHCDCKNVMNMSTMWTGWYNMBENVSQDMHY	79		
Oy	987	ttccgcagaaggtctgacctg-tggatatttlttgtagacactccaagaaccgctaata	1045		
Dd	80	MBVINTKADVCNH-TRCSRMRYBTAPMAHYDNYCNBAYNNNDYHMHBMYBNTGCMTCT	138		
Oy	1046	caactccaaaacglttttgacccctcccacaacgcccccctcccccccatccttcgcgt	1105		
Dd	139	MMCBMHNKTKTASGMHTSTNYDKRSSTNTWGVTBSYDKSMHQWCSSBVKKYHTVFSTR	198		
Oy	1106	caagcatgtgtcccaactcgctcctctgcgcagtctgttcccaactgtatttccctcgcgc	1165		
Dd	199	ATRSYTGVRRKYCVMMMTKKVKYKKYHHVBSCBH	231		
Oy	1166	gcgaatctcglttgaggaggaagcgaggaactg	1198		

RESULT	2								
LOCUS	AA754459	252 bp	mRNA	EST	20-JAN-1998				
DEFINITION	97SN1787 Rice Immature Seed Lambda ZAPII cDNA Library Oriza sativa								
ACCESSION	97SN1787								
NCBI	AA754459								
VERSION	97801165								
KEYWORDS	AA754459.1	GI:2801165							
SOURCE	EST.								
ORGANISM	Oriza sativa.								
	Oriza sativa								
	Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;								
	euphyllophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales;								
	Poaceae; Oryza.								
REFERENCE	1 (bases 1 to 252)								
AUTHORS	Nahm,B.H., Kim,J.K., Cheong,J.J., Kim,S.I., Hahn,T.R., Moon,E.P.,								
	Kim,W.T., Kim,M.Y., Yang,M.S., Park,R.D., Sohn,U.I., Kang,K.Y.,								
	Ise,M.C. and Eun,M.Y.								
TITLE	Large-scale Sequencing Analysis of ESTs from Rice Immature Seed								
JOURNAL	Unpublished (1998)								
COMMENT	On Jan 14, 1998 this sequence version replaced gi:1797457.								

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Submitted by Baek Hie Namh, Dept of Biological Science, Myongji
University, Yongin, Korea. 449-728 bhnamh@bloserver.myongji.ac.kr
Seq primer: M13 Reverse Primer.
Location/Qualifiers
1. 252

/note="vector: pBluescript SK(+); Site_1: EcoRI; Site_2: XhoI; Directional cDNA library inserted into lambda ZapIII vector at 5' end with EcoRI and 3' end with Xho I site."

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/db_xref="taxon:4530"
/map="6"
/clone="97SN1787"
/clone_1lb="Rice Immature Seed Lambda ZapIt cDNA Library"
/issue_type="Immature Seed"
/dev_stage="5 days after pollination"
/lab_host="E. coli SOLR"
BASE COUNT      5 a      21 c      12 g      35 t      179 others
ORIGIN
Query Match      2.1%; Score 59; DB 17; Length 252;
Best Local Similarity 13.9%; Pred. No. 1.04e-50;
Matches          32; Conservative 114; Mismatches 80; Indels 4; Gaps 4;

```

[illegible][illegible]

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Submitted by Baek Hie Nahm, Dept of Biological Science, Myongji
University, Yongin, Korea. 449-728 bhna@bioserver.myongji.ac.kr
Seq primer: M13 Reverse Primer.
LOCATION/QUALIFIERS
1. 247

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/clone_lib="Rice Immature Seed Lambda ZAPIT CDNA Library"
/clone="97SN1784"
/map="6"
/seq_attr="cannon.7500"

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Query Match	1.7%;	Score 49;	DB 17;	Length 247;
Best Local Similarity	12.2%;	Pred. No. 3.91e-35;		

Query Match	1.6%	Score 44	DB 27	Length 656
Best Local Similarity	63.1%	Pred. 1.0e-27		
Matches	142	Conservative	0	Mismatches 80; Indels 3; Gaps 2
Db	301	TTTTCTGCATCACTTTTCTGAGATCTGACTGTGAGAGATCTGACTGTAGAGAAAT	360	
Cp	1482	ttttctaaagaatttttttaagatcttaattttctagatatacttagctgcacagagaat	1423	
Db	361	ATGAGTATCGTGGCATTACTGCAAAAGAAAATTAAGTGTGCAAAAGTTTCAGATCT	420	

Query Match	1.08;	Score 29;	DB 27;	Length 308;
Best Local Similarity	79.68;	Pred. No. 1.20e-07;		
Matches	39;	Conservative	0;	Mismatches 10;
			Indels 0;	Gaps 0;

Db 242 ACCATTAAAAATTACATGCCACGAAACATTAAATTATTAATTTTAAATATACGTAA 2988
||| ||||| ||| ||| ||||| ||| ||| ||||| ||| |||
QY 114 acaaaaaaatcaccagcctcaacaacattacaatatgatccaanaatagacactaa 1700

FEATURES
Source

Query Match	1.08;	Score 27;	DB 10;	Length 315;
Best Local Similarity	67.5%;	Pred. No. 2.38e-05;		
Matches	52;	Mismatches 25;	Indels 0;	Gaps 0;

RESULT	14			
LOCUS	W29651	351 bp	mRNA	EST
DEFINITION	mc07b09.r1 Soares mouse p33MF19.5			11-SEP-1996
ACCESSION	IMAGE:347791 5', mRNA sequence.			
NID	W29651			
VERSION	9130984.8			
KEYWORDS	W29651.1	GI:1309818		
	EST.			

FEATURES
source

Query Match	1.0%;	Score 27;	DB 34;	Length 351;
Best Local Similarity	75.5%;	Pred. No. 2.38e-05;		
Matches	40;	Conservative	0;	Mismatches 13; Indels 0; Gaps 0

LOCUS	15	A0445618	372 bp	DNA	GSS	30-MAR-1999
DEFINITION		GSSSTC00106 Trypanosoma cruzi random genomic library Trypanosomacruzi genomic clone G10f4 5' , genomic survey sequence.				
ACCESSION		A0445618				
NID		94554839				
VERSION		A0445618.1	GI:4554839			

ORGANISM
Trypanosoma cruzi
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma; Schizocrypanum.
REFERENCE
1 (bases 1 to 372)
AUTHORS
Sanchez, D.O.
TITLE
Trypanosoma cruzi random genomic sequences
JOURNAL
Unpublished (1999)
COMMENT

Contact: Sanchez D.O.
 Instituto de Investigaciones Biotecnologicas (Univ. Nac. de Gral
 San Martin)
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 Tel: (54-11)4752-0021
 Fax: (54-11)4752-9639
 Email: dsanchez@inti.gov.ar
 Seq primer: T7
 Class: Shocgun.

FEATURES

source
 1. .372
 Location/Qualifiers
 /organism="Trypanosoma cruzi"
 /strain="Cl-Brenner"
 /note="Vector: PBS(-) (PHARMACIA)"
 /db_xref="taxon:5693"
 /clone="G10F4"
 /clone_lib="Trypanosoma cruzi random genomic library"
 /cell_type="epimastigote"
 BASE COUNT 86 a 44 c 58 g 73 t 111 others
 ORIGIN

Query Match 1.0%; Score 27; DB 42; Length 372;

Best Local Similarity 27.6%; Pred. No. 2,38e-05;

Matches 16; Conservative 26; Mismatches 16; Indels 0; Gaps 0;

Db 2 YSGATTTRKMYTGAMRYSGAKRACCMWCCTWKYKTGRCGYNAYGAAMRACKGKRRM 59

Cp 1375 tggtttaggttagaacgacgtgacgtcttcctacgtgcgacttaagaataatataca 1318

Search completed: Tue Dec 28 20:25:08 1999
 Job time : 10144 secs.